



SEQ ID NO: 116

Sequences producing significant alignments:

		Score	E	
		(bits)	Value	
gi 38565928 gb AAH62099.1	Unknown (protein for MGC:69652) ...	66	1e-10	
gi 38073248 gb AAR10808.1	brain-specific K-Cl cotransporte...	66	1e-10	
gi 38073246 gb AAR10807.1	K-Cl cotransporter KCC3a isoform...	66	1e-10	
gi 38073244 gb AAR10806.1	K-Cl cotransporter KCC3b isoform...	66	1e-10	
gi 34856648 ref XP_342490.1	similar to K-Cl cotransporter ...	66	1e-10	G
gi 33329256 gb AAQ10028.1	K-Cl cotransporter KCC3a-S2 isof...	66	1e-10	G
gi 33329252 gb AAQ10026.1	K-Cl cotransporter KCC3a-X2M iso...	66	1e-10	G
gi 22416428 gb AAM96216.1	potassium-chloride transporter-3...	66	1e-10	G
gi 22416427 gb AAM96215.1	potassium-chloride transporter-3...	66	1e-10	G
gi 41281645 ref NP_598410.1	solute carrier family 12, memb...	66	1e-10	G
gi 19526769 ref NP_598409.1	solute carrier family 12, memb...	66	1e-10	G
gi 47124056 gb AAH70107.1	SLC12A6 protein [Homo sapiens]	66	1e-10	G
gi 6693798 gb AAF24986.1	K-Cl cotransporter KCC3 [Homo sap...	66	1e-10	G
gi 7268880 emb CAB79084.1	reticuline oxidase-like protein ...	33	0.63	G

gi 23487079 gb EAA20955.1	gamma-glutamylcysteine synthetas...	31	2.8	
gi 33865772 ref NP_897331.1	putative methionine synthase [...	31	3.7	G
gi 34397598 gb AAQ66660.1	FtsK/SpoIIIE family protein [Por...	31	3.7	G
gi 45512893 ref ZP_00164459.1	COG1410: Methionine synthase...	31	3.7	
gi 23619116 ref NP_705078.1	DNA replication licensing fact...	30	5.0	G
gi 11559506 gb AAG37988.1	DNA replication licensing factor...	30	5.0	
gi 51473445 ref YP_067202.1	Alanine-adding enzyme.; L-Ala ...	29	8.9	G
gi 15892254 ref NP_359968.1	UDP-N-acetylmuramate--alanine ...	29	8.9	G
gi 15604117 ref NP_220632.1	UDP-N-ACETYLMURAMATE--ALANINE ...	29	8.9	G
gi 42453471 ref ZP_00153378.1	hypothetical protein Rick032...	29	8.9	
gi 21554228 gb AAM63303.1	unknown [Arabidopsis thaliana]	29	8.9	
gi 28262111 gb EAA25615.1	UDP-N-acetylmuramate--alanine li...	29	8.9	
gi 18026640 gb AAL55556.1	phospholipase A2 [Lapemis hardwi...	29	8.9	
gi 18000323 gb AAL54920.1	PLA2 [Lapemis hardwickii] >gi 26...	29	8.9	
gi 129509 sp P00610 PA2 ENHSC	Phospholipase A2 (Myotoxin) (...	29	8.9	
gi 12323245 gb AAG51597.1	hypothetical protein; 76801-7830...	29	8.9	G
gi 39997987 ref NP_953938.1	ankyrin-related protein [Geoba...	29	12	G
gi 23508289 ref NP_700958.1	hypothetical protein [Plasmodi...	29	16	G
gi 23509774 ref NP_702441.1	hypothetical protein [Plasmodi...	29	16	G
gi 32411321 ref XP_326141.1	predicted protein [Neurospora ...	29	16	G
gi 52209942 emb CAH35914.1	putative multidrug resistance p...	29	16	
gi 17861422 gb AAL39188.1	GH0419lp [Drosophila melanogaster]	28	22	
gi 33863001 ref NP_894561.1	putative methionine synthase [...	28	22	G
gi 23509969 ref NP_702636.1	hypothetical protein [Plasmodi...	28	22	G
gi 16331640 ref NP_442368.1	5-methyltetrahydrofolate--homo...	28	22	G
gi 50751208 ref XP_426633.1	PREDICTED: similar to DBCCR1-1...	28	22	G
gi 50424887 ref XP_461033.1	unnamed protein product [Debar...	28	22	G
gi 48891299 ref ZP_00324839.1	COG1410: Methionine synthase...	28	22	
gi 45526435 ref ZP_00177640.1	COG1410: Methionine synthase...	28	22	
gi 24641567 ref NP_572812.2	CG32654-PC [Drosophila melanog...	28	22	G
gi 15672097 ref NP_266271.1	preprotein translocase subunit...	28	29	G
gi 18033725 gb AAL57226.1	gamma-glutamylcysteine synthetas...	28	29	
gi 50259358 gb EAL22031.1	hypothetical protein CNBC1690 [C...	28	29	
gi 23957767 ref NP_473309.2	transporter, putative [Plasmod...	28	29	G
gi 50305315 ref XP_452617.1	unnamed protein product [Kluyv...	28	29	G
gi 8778246 gb AAF79255.1	F12K21.9 [Arabidopsis thaliana]	28	29	
gi 4713921 gb AAD28293.1	gamma-glutamylcysteine synthetase...	28	29	
gi 13384201 gb AAK21311.1	myosin subfamily XI heavy chain ...	28	29	
gi 4587527 gb AAD25758.1	Strong similarity to F19I3.2 gi 3...	28	29	G
gi 18399342 ref NP_564449.1	FAD-binding domain-containing ...	28	29	G
gi 23508909 ref NP_701577.1	hypothetical protein [Plasmodi...	27	39	G
gi 46444561 gb EAL03835.1	hypothetical protein CaO19.1532 ...	27	39	
gi 23510149 ref NP_702815.1	hypothetical protein [Plasmodi...	27	39	G
gi 23510013 ref NP_702679.1	hypothetical protein [Plasmodi...	27	39	G
gi 50419097 ref XP_458071.1	unnamed protein product [Debar...	27	39	G
gi 6910587 gb AAF31292.1	CDS [Arabidopsis thaliana]	27	39	
gi 28933053 emb CAD28639.1	NADH dehydrogenase subunit 1 [E...	27	39	
gi 42562475 ref NP_174582.3	no apical meristem (NAM) famil...	27	39	G
gi 42571727 ref NP_973954.1	no apical meristem (NAM) famil...	27	39	G
gi 23490643 gb EAA22371.1	hypothetical protein [Plasmodium...	27	39	
gi 23487445 gb EAA21055.1	acetyl-CoA carboxylase 1 precurs...	27	39	

gi 23485391 qb EAA20406.1 	XPG I-region, putative [Plasmodi...	27	39
gi 23484327 qb EAA19697.1 	hypothetical protein [Plasmodium...	27	39
gi 23509627 ref NP_702294.1 	hypothetical protein [Plasmodi...	27	52 G
gi 23612180 ref NP_703760.1 	hypothetical protein [Plasmodi...	27	52 G
gi 32394494 qb AAM93945.1 	peptidoglycan binding domain pro...	27	52
gi 23613387 ref NP_703231.1 	hypothetical protein [Plasmodi...	27	52 G
gi 49119233 qb AAH73236.1 	MGC80568 protein [Xenopus laevis]	27	52 G
gi 50550261 ref XP_502603.1 	hypothetical protein [Yarrowia...	27	52 G
gi 46227257 qb EAK88207.1 	Low complexity hypothetical prot...	27	52
gi 47206405 emb CAG01534.1 	unnamed protein product [Tetrao...	27	52
gi 23488127 qb EAA21236.1 	maeb1 [Plasmodium yoelii yoelii]	27	52
gi 23483880 qb EAA19400.1 	hypothetical protein [Plasmodium...	27	52
gi 19075192 ref NP_587692.1 	possible sexual cycle protein ...	27	70 G
gi 23619193 ref NP_705155.1 	hypothetical protein [Plasmodi...	27	70 G
gi 23619000 ref NP_704962.1 	hypothetical protein [Plasmodi...	27	70 G
gi 38566630 qb AAR24205.1 	Atlg30730 [Arabidopsis thaliana]...	27	70
gi 23612548 ref NP_704109.1 	hypothetical protein [Plasmodi...	27	70 G
gi 23612852 ref NP_704391.1 	hypothetical protein [Plasmodi...	27	70 G
gi 29345560 ref NP_809063.1 	putative ferric aerobactin rec...	27	70 G
gi 33115103 qb AAP95014.1 	putative histone deacetylase [Co...	27	70
gi 30793778 tpg DAA01304.1 	TPA: homeodomain protein ECHD-1...	27	70 G
gi 19112371 ref NP_595579.1 	putative alpha-1,2-galactosylt...	27	70 G
gi 39979638 ref NP_950252.1 	DBCCR1-like [Homo sapiens] >gi...	27	70 G
gi 46442684 qb EAL01971.1 	hypothetical protein CaO19.13822...	27	70
gi 46443217 qb EAL02500.1 	conserved hypothetical protein [...]	27	70
gi 46443017 qb EAL02302.1 	hypothetical protein CaO19.8490 ...	27	70
gi 46442889 qb EAL02175.1 	hypothetical protein CaO19.871 [...]	27	70
gi 23957712 ref NP_473166.2 	hypothetical protein, conserve...	27	70 G
gi 50759954 ref XP_425787.1 	PREDICTED: similar to ornithin...	27	70 G
gi 50755874 ref XP_414920.1 	PREDICTED: similar to Elongati...	27	70 G
gi 50421145 ref XP_459118.1 	unnamed protein product [Debar...	27	70 G
gi 50365429 ref YP_053854.1 	alanyl-tRNA synthetase [Mesopl...	27	70 G
gi 28829605 qb AAO52122.1 	similar to Plasmodium falciparum...	27	70
gi 28829852 qb AAO52354.1 	similar to Dictyostelium discoid...	27	70
gi 4587529 qb AAD25760.1 	Strong similarity to F19I3.2 gi 3...	27	70 G

Alignments

☐ >gi|38565928|qb|AAH62099.1| Unknown (protein for MGC:69652) [Mus musculus]
 Length = 1106

Score = 65.5 bits (147), Expect = 1e-10
 Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
 KKARNAYLNNSNYEEGDEY
 Sbjct: 95 KKARNAYLNNSNYEEGDEY 113

☐ >gi|38073248|gb|AAR10808.1| brain-specific K-Cl cotransporter KCC3a isoform [Rat]
Length = 156

Score = 65.5 bits (147), Expect = 1e-10
Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
KKARNAYLNNSNYEEGDEY
Sbjct: 85 KKARNAYLNNSNYEEGDEY 103

☐ >gi|38073246|gb|AAR10807.1| K-Cl cotransporter KCC3a isoform [Rattus norvegicus]
Length = 171

Score = 65.5 bits (147), Expect = 1e-10
Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
KKARNAYLNNSNYEEGDEY
Sbjct: 100 KKARNAYLNNSNYEEGDEY 118

☐ >gi|38073244|gb|AAR10806.1| K-Cl cotransporter KCC3b isoform [Rattus norvegicus]
Length = 95

Score = 65.5 bits (147), Expect = 1e-10
Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
KKARNAYLNNSNYEEGDEY
Sbjct: 24 KKARNAYLNNSNYEEGDEY 42

☐ >gi|34856648|ref|XP_342490.1| ☒ similar to K-Cl cotransporter 3b [Rattus norvegi]
Length = 1094

Score = 65.5 bits (147), Expect = 1e-10
Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
KKARNAYLNNSNYEEGDEY
Sbjct: 44 KKARNAYLNNSNYEEGDEY 62

☐ >gi|33329256|gb|AAQ10028.1| ☒ K-Cl cotransporter KCC3a-S2 isoform [Homo sapiens]
gi|33329254|gb|AAQ10027.1| ☒ K-Cl cotransporter KCC3a-S1 isoform [Homo sapiens]
Length = 1091

Score = 65.5 bits (147), Expect = 1e-10
Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19

KKARNAYLNNSNYEEGDEY
Sbjct: 51 KKARNAYLNNSNYEEGDEY 69

☐ >gi|33329252|gb|AAQ10026.1| ☒ K-Cl cotransporter KCC3a-X2M isoform [Homo sapiens]
Length = 1135

Score = 65.5 bits (147), Expect = 1e-10
Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
KKARNAYLNNSNYEEGDEY
Sbjct: 95 KKARNAYLNNSNYEEGDEY 113

☐ >gi|22416428|gb|AAM96216.1| potassium-chloride transporter-3b [Homo sapiens]
gi|4826780|ref|NP_005126.1| ☒ potassium chloride cotransporter KCC3; agenesis of
callosum and peripheral neuropathy (Andermann syndrome)
[Homo sapiens]
gi|4585229|gb|AAD25337.1| ☒ K:Cl cotransporter 3 [Homo sapiens]
Length = 1099

Score = 65.5 bits (147), Expect = 1e-10
Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
KKARNAYLNNSNYEEGDEY
Sbjct: 59 KKARNAYLNNSNYEEGDEY 77

☐ >gi|22416427|gb|AAM96215.1| ☒ potassium-chloride transporter-3a [Homo sapiens]
gi|5106523|gb|AAD39742.1| ☒ K-Cl cotransporter KCC3a [Homo sapiens]
gi|27151690|sp|Q9UHW9|S126 HUMAN ☒ Solute carrier family 12 member 6 (Electroneut
potassium-chloride cotransporter 3) (K-Cl cotransporter
3)
Length = 1150

Score = 65.5 bits (147), Expect = 1e-10
Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
KKARNAYLNNSNYEEGDEY
Sbjct: 110 KKARNAYLNNSNYEEGDEY 128

☐ >gi|41281645|ref|NP_598410.1| ☒ solute carrier family 12, member 6 [Mus musculus]
gi|15042077|gb|AAK81895.1| ☒ K-Cl cotransporter 3a [Mus musculus]
gi|27151686|sp|Q924N4|S126 MOUSE Solute carrier family 12 member 6 (Electroneutra
potassium-chloride cotransporter 3) (K-Cl cotransporter
3)
Length = 1150

Score = 65.5 bits (147), Expect = 1e-10

Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
 KKARNAYLNNSNYEEGDEY
 Sbjct: 110 KKARNAYLNNSNYEEGDEY 128

☐ >gi|19526769|ref|NP_598409.1| ☒ solute carrier family 12, member 6 [Mus musculus]
 gi|15042079|gb|AAK81896.1| ☒ K-C1 cotransporter 3b [Mus musculus]
 Length = 1099

Score = 65.5 bits (147), Expect = 1e-10
 Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
 KKARNAYLNNSNYEEGDEY
 Sbjct: 59 KKARNAYLNNSNYEEGDEY 77

☐ >gi|47124056|gb|AAH70107.1| ☒ SLC12A6 protein [Homo sapiens]
 Length = 1156

Score = 65.5 bits (147), Expect = 1e-10
 Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
 KKARNAYLNNSNYEEGDEY
 Sbjct: 116 KKARNAYLNNSNYEEGDEY 134

☐ >gi|6693798|gb|AAF24986.1| ☒ K-C1 cotransporter KCC3 [Homo sapiens]
 Length = 1150

Score = 65.5 bits (147), Expect = 1e-10
 Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 KKARNAYLNNSNYEEGDEY 19
 KKARNAYLNNSNYEEGDEY
 Sbjct: 110 KKARNAYLNNSNYEEGDEY 128

☐ >gi|7268880|emb|CAB79084.1| ☒ reticuline oxidase-like protein [Arabidopsis thaliana]
 gi|5262224|emb|CAB45850.1| ☒ reticuline oxidase-like protein [Arabidopsis thaliana]
 gi|7488296|pir|T10626 ☒ reticuline oxidase homolog F21C20.190 - Arabidopsis thaliana
 gi|15233416|ref|NP_193816.1| ☒ FAD-binding domain-containing protein [Arabidopsis thaliana]
 Length = 539

Score = 33.3 bits (71), Expect = 0.63
 Identities = 14/32 (43%), Positives = 15/32 (46%), Gaps = 14/32 (43%)

Query: 1 KKARNAYLN-----NSNYEEGDEY 19
 K RNAYLN NS YEEG+ Y
 Sbjct: 471 KNPRNAYLNRYRDVDIGVNDHGTNS-YEEGEVY 501

☐ >gi|23487079|gb|EAA20955.1| gamma-glutamylcysteine synthetase-related [Plasmodiu
yoelii]
Length = 999

Score = 31.2 bits (66), Expect = 2.8
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 10 NSNYEEGDEY 19
N+NYEE DEY
Sbjct: 973 NTNYEESDEY 982

Score = 18.9 bits (37), Expect = 13906
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 5 NAYLNNS 11
N +LNNS
Sbjct: 151 NVFLNNS 157

☐ >gi|33865772|ref|NP_897331.1| ☒ putative methionine synthase [Synechococcus sp.
gi|33632942|emb|CAE07753.1| ☒ putative methionine synthase [Synechococcus sp. WH
Length = 1209

Score = 30.8 bits (65), Expect = 3.7
Identities = 8/11 (72%), Positives = 11/11 (100%)

Query: 8 LNNSNYEEGDE 18
LN++NYE+GDE
Sbjct: 459 LNSTNYEDGDE 469

☐ >gi|34397598|gb|AAQ66660.1| ☒ FtsK/SpoIIIE family protein [Porphyromonas gingiva
gi|34541282|ref|NP_905761.1| ☒ FtsK/SpoIIIE family protein [Porphyromonas gingiva
Length = 861

Score = 30.8 bits (65), Expect = 3.7
Identities = 10/22 (45%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 7 YLNNSNYEEG-----DEY 19
YLNNS YE+G D+Y
Sbjct: 298 YLNNSEYEDGPAGESADDPDDY 319

☐ >gi|45512893|ref|ZP_00164459.1| COG1410: Methionine synthase I, cobalamin-bindin
[Synechococcus elongatus PCC 7942]
Length = 1190

Score = 30.8 bits (65), Expect = 3.7
Identities = 8/11 (72%), Positives = 11/11 (100%)

Query: 8 LNNSNYEEGDE 18
LN++NYE+GDE
Sbjct: 447 LNSTNYEDGDE 457

☐ >gi|23619116|ref|NP_705078.1| ☒ DNA replication licensing factor mcm4, putative
falciparum 3D7]
gi|23615323|emb|CAD52314.1| ☒ DNA replication licensing factor mcm4, putative [Pl
falciparum 3D7]
Length = 1005

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/11 (72%), Positives = 10/11 (90%)

Query: 8 LNNSNYEEGDE 18
LNN+NYE+ DE
Sbjct: 187 LNNTNYEDDDE 197

Score = 20.6 bits (41), Expect = 4290
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 7 YLNNSN 12
YLN+SN
Sbjct: 784 YLNDSN 789

Score = 18.5 bits (36), Expect = 18658
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 7 YLNNSN 12
YLN SN
Sbjct: 64 YLNQSN 69

☐ >gi|11559506|gb|AAG37988.1| DNA replication licensing factor MCM4 [Plasmodium fa
Length = 1005

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/11 (72%), Positives = 10/11 (90%)

Query: 8 LNNSNYEEGDE 18
LNN+NYE+ DE
Sbjct: 187 LNNTNYEDDDE 197

Score = 20.6 bits (41), Expect = 4290
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 7 YLNNSN 12
YLN+SN
Sbjct: 784 YLNDSN 789

Score = 18.5 bits (36), Expect = 18658
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 7 YLNNSN 12
 YLN SN
Sbjct: 64 YLNQSN 69

☐ >[gi|51473445|ref|YP_067202.1|](#) ☒ Alanine-adding enzyme.; L-Ala ligase.; L-alanine MurC synthetase.; UDP-MurNAC:L-alanine ligase.;
UDP-N-acetylmuramate--L-alanine ligase;
UDP-N-acetylmuramoyl-L-alanine synthetase.;
UDP-N-acetylmuramoylalanine synthetase.;
UDP-N-acetylmuramyl:L-alanine ligase.;
UDP-acetylmuramyl-L-alanine synthetase.;
UDPMurNAC-L-alanine synthetase.; Uridine
5prime-diphosphate-N-acetylmuramyl-L-alanine
synthetase.; Uridine diphosphate
N-acetylmuramate:L-alanine ligase.; Uridine
diphospho-N-acetylmuramoylala>

[gi|51459757|gb|AAU03720.1|](#) ☒ UDP-N-acetylmuramate--L-alanine ligase [Rickettsia t
Wilmington]
Length = 498

Score = 29.5 bits (62), Expect = 8.9
Identities = 11/19 (57%), Positives = 13/19 (68%), Gaps = 2/19 (10%)

Query: 2 KARNAYLNNSNY--EEGDE 18
 K+ NAYL +SNY E DE
Sbjct: 153 KSTNAYLGSSNYLIAEADE 171

☐ >[gi|15892254|ref|NP_359968.1|](#) ☒ UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8
conorii str. Malish 7]

[gi|15619392|gb|AAL02869.1|](#) ☒ UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8] [R
conorii str. Malish 7]

[gi|20532173|sp|Q92IT9|MURC_RICCN](#) UDP-N-acetylmuramate--L-alanine ligase
(UDP-N-acetylmuramoyl-L-alanine synthetase)

[gi|25293603|pir||C97741](#) hypothetical protein murC [imported] - Rickettsia conorii
Malish 7)
Length = 485

Score = 29.5 bits (62), Expect = 8.9
Identities = 11/19 (57%), Positives = 13/19 (68%), Gaps = 2/19 (10%)

Query: 2 KARNAYLNNSNY--EEGDE 18
 K+ NAYL +SNY E DE
Sbjct: 153 KSTNAYLGSSNYLIAEADE 171

☐ >[gi|15604117|ref|NP_220632.1|](#) ☒ UDP-N-ACETYLMURAMATE--ALANINE LIGASE (murC) [Ric
str. Madrid E]

[gi|3860809|emb|CAA14709.1|](#) ☒ UDP-N-ACETYLMURAMATE--ALANINE LIGASE (murC) [Rickett
[gi|6225734|sp|Q9ZDS8|MURC_RICPR](#) UDP-N-acetylmuramate--L-alanine ligase